

Fig. 1

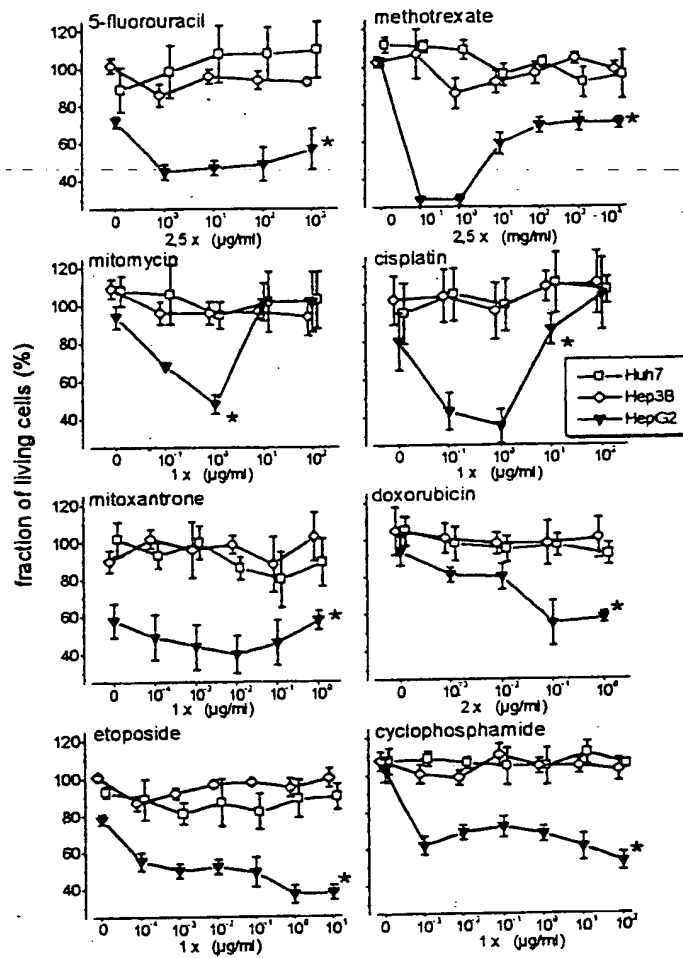


Fig. 2

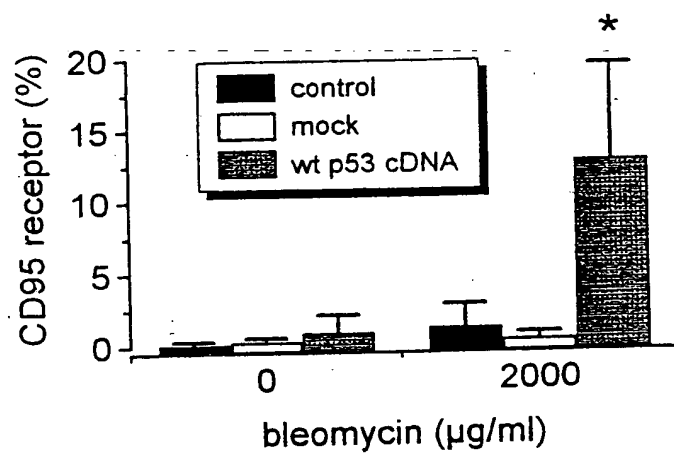


Fig. 3

4/26

620 GATCCCGCTGGGCAGGCGGG 640 GCAGTCCGGCGCTCCTCGG 660 AGACCACTGCGCTCCACGTT
Sau3A1
 680 GAGGTGGGCGTGGGGGGCGG 700 ACAGGAATTGAAGCGGAAGT 720 CTGGGAAGCTTTAGGGTCGC
HindIII
 740 TGGAGGGGGACCCCGGTTGG 760 AGAGAGGAGCGGAACCTCTG - GACAAGCCCTGACAAGCCAA
p53BE
 800 GCCAAAGGTCCGCTCCGGCG 820 CGGGTGGGTGAGTGC GCGCC 840 GCCCCGCGGGGCGGGGAGA
 860 GAGCCTGCAGCCTTCAGAAC 880 AGATAT

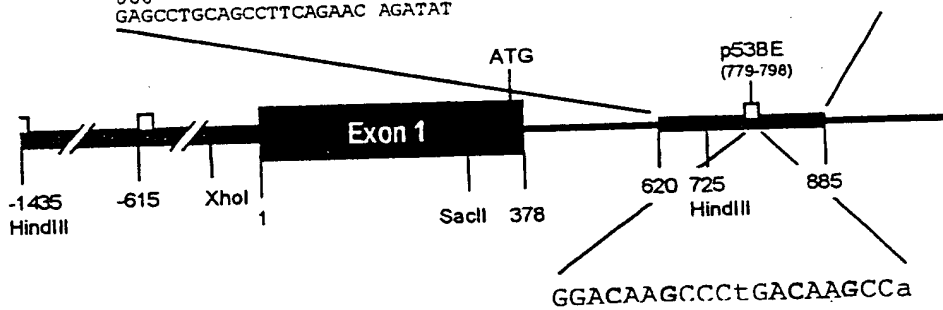


Fig. 4

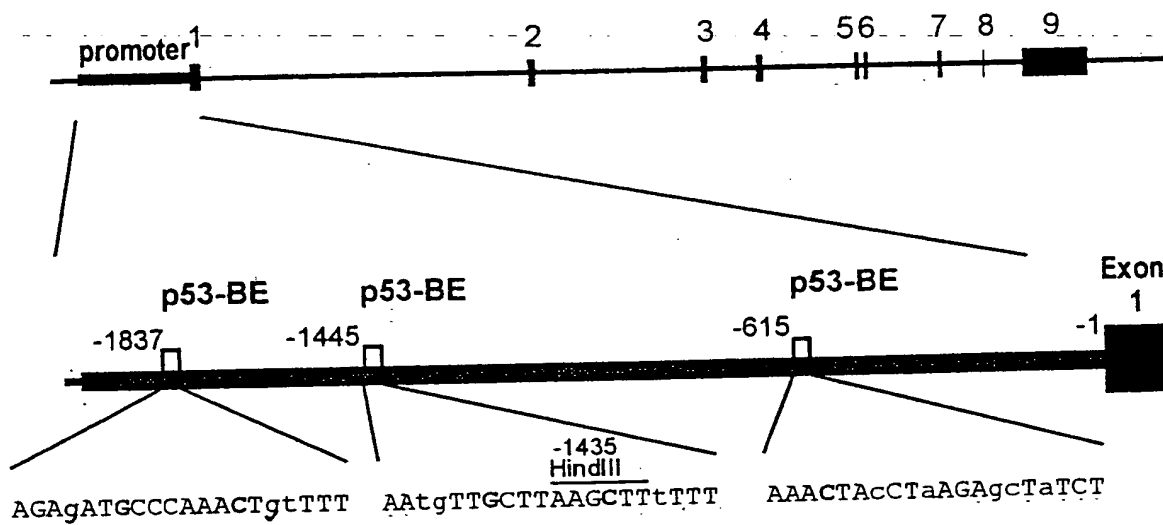


Fig. 5

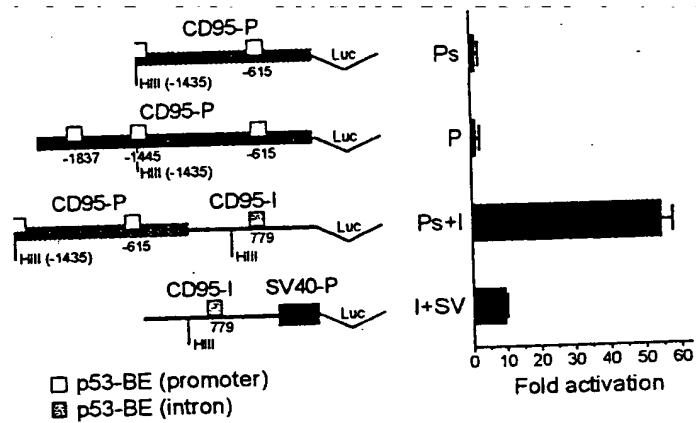


Fig. 6

GATCCCGCTGGGCAGGCGGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CTAGGGCGACCCGTCGCCCGTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA

GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC
61 -----+-----+-----+-----+-----+-----+-----+ 120
CTCCACCCGACCCCCCGCCTGTCCTTAACCTTCGCCTTCAGACCCTTCGAAATCCCAGCG

<---- 4. P53-BE ---->
(intron)

TGGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGACAGCCCTGACAGCCAA
121 -----+-----+-----+-----+-----+-----+-----+ 180
ACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCTGGGACTGTTCTGGTT

GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGCGGGGAGA
181 -----+-----+-----+-----+-----+-----+-----+ 240
CGGTTTCCAGGCGAGGCCGCGCCCACCCACTCACGCGCGGCGGGGCGCCCCGCCCTCT

GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA
241 -----+-----+-----+-----+-----+-----+-----+ 300
CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTTT

TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT
301 -----+-----+-----+-----+-----+-----+-----+ 360
ATTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAAAGAAA

CTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT
361 -----+-----+-----+-----+-----+-----+-----+ 420
GAGCTTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA

GTCACACAGAAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTA
421 -----+-----+-----+-----+-----+-----+-----+ 480
CAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT

AGTCGCTGCCTGAGTGGTTTTATTTTGTGTTTTGTTTTCTGCCCTTCTCTTTCTTTTGG
481 -----+-----+-----+-----+-----+-----+-----+ 540
TCAGCGACGGACTACCAAAGTAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAC

CCCTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
541 -----+-----+-----+-----+-----+-----+-----+ 600
GGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCCAACCACC

TACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCT
601 -----+-----+-----+-----+-----+-----+-----+ 660
ATGAGCAAGGTTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTCCGA

GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAGAGACGTG
661 -----+-----+-----+-----+-----+-----+-----+ 720
CAAACTTTTCAGGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTTCTCTGCAC

TCAGTGTGCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT

Fig. 8

2nd half of the
2.p53-BE
(promoter)

AGCTTTTGGCTACATTTTTTATTGTAAAG
448 -----+----- 480
TCGAAAAACCGATGTAAAAAATAACATTTC

TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
481 -----+----- 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTTCATAATTCATTCTCTAG

CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
541 -----+----- 600
GTGTATACTCAACGACCGAATATTAAGTGTGAGTTCCTATGACTAAAACAGTTAACA

CCTTTCCCTTTTTTCTCTCTCCCTCCTTCATTCTCTCTCCCTTACCTCTCCTTC
601 -----+----- 660
GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAAG

CTTCCCTCACACCCCTTTTCTCTCTCTTTTACATTTTTTTATTAAATGAACCTTTTC
661 -----+----- 720
GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTTACTTGAAAAG

ATTTTGAATAGTTTTAGGATTTCAAAAAATTGTCAGAGATAATACAGAGAATGCCATA
721 -----+----- 780
TAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

TACCATCCTCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
781 -----+----- 840
ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

GGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
841 -----+----- 900
CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTGAGATGACTTTCCACCTTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
901 -----+----- 960
TGTTGCGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTTGTGTCC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAACAGGCTCCA
991 -----+----- 1020
CACTACCTTTGCGGAGTCTCCCATTTGGATTGGATCTAAACTCCCGGGTTTGTCCGAGGT

GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
1021 -----+----- 1080
CTTCTTTTACAGTTGACTCTCTTCGGACTTCCTACTTGTACCCCGATTTCGTTTCCCAAT

Downloaded from www.jstor.org

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1081 -----+-----+-----+-----+-----+-----+-----+ 1140
AATTACACAATAATTACCCAACTTAGATTAACCCTTCCCTCTCTCCAACGTCTCACTCCA
GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
CGTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTT
CTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATACTTCTGTAAAATT
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
GACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

←--- 3.p53-~~BE~~ ----→
(promoter)

[illegible][illegible]

1921 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCCTGACCACCGGGGC
 1980 GGAGGGGTTGGGCCCCGCAAGGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG
 1981 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
 2040 AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA
 2041 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG
 2100 GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGAC
 2101 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGC
 2160 CGTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG
 2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTA
 2220 CCTGTACATGTCTCGAGCTCTTCATGATCACCAGGTGCACCCGGCACGTGGAATTCGAAT
 ←---4.p53-BE---
 (intron)
 2221 GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGGACAAGCCCTGAC
 2280 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG
 ----->
 2281 AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC
 2340 TTCGGTTCGGTTTTCCAGGCGAGGCCGCGCCACCCACTCAGCGCGGCGGGGCGCCCCG
 2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACG
 2400 CCCCTCTCTCGGACGTCGGAAGTCTTGTCTATAACGAGTAAAAGACCGTCAAGAGTCTGC
 2401 TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAAGGCACCT
 2460 ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA
 2461 TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
 2520 AAAGAAAGAGCTTTTTCAATATAACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA
 2521 TTTTATTGTCAACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAA
 2580 AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT
 2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTCTGCCCCTTCTCTTTCT
 2640 CTGACATTACGCGACGGACTACCPAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA
 2641 TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG
 2700 AGAAAACGGGAAAGAATCGAACGTGAGGGTACCATAAAGACGAACAGAGGACGACCCC

2701 TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
-----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCCGCGGATAATAACCGGTTCTTTGAACT

2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
-----+-----+-----+-----+ 2820
CGTCGGACAAAACCTTTTCAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

2821 AGACGTG
----- 2827
TCTGCAC

T02F40-T624E860

Fig. 9

1 TGAGGACTCTCAGGAATATGCTGGTAAAAATAAAAATAACCTTTAGAGATGCCCAAAGTGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
ACTCCTGAGAGTCCCTTATACGACCATTTTATTTTATTGGAATCTCTACGGGTTTGACA

-->

61 TTTCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTTCAAAGGATTCCA 120
- - - - -
AAAGGGGTCTTGTTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT - -

121 AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCCTTTGACATTAGCATAC
-----+-----+-----+-----+-----+-----+-----+-----+ 180
TTCCGTTTCTTCAAACCCCTTGTCATATATATTAATGGGTTGGGAAACTGTAATCGTATG

181 TAAGGGCCCTGAGAAGTTTGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT 240
-----+-----+-----+-----+-----+
ATTCCCGGGACTCTTCAAAACCTAATTCTTCAAAGTTTAATTTTCATTGGGTCTTAAAA

241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT 300
GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA

301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGGTATGGCATAGA 360
-----+-----+-----+-----+-----+-----+
CTTGAACCTCTATTAATCTGCATGCCCATCTCCCATCCCCCTCCCCCATACCGTATCT

361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA
-----+-----+-----+-----+-----+-----+-----+-----+ 420
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<--- 2.p53-BE --->

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTTATTTGTAAAG
-----+-----+-----+-----+-----+-----+-----+ 480
TGATTGGTAGAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAAATAAACATTTTC

481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
+-----+-----+-----+-----+-----+-----+ 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTTCATAATTCATTCCCTTCTAG

541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT 600
-----+-----+-----+-----+-----+
GTGTATACACTCAACGACCGAATATTAAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA

601 CCTTTCCTTTTCTCTTCCCTCCTTCCATTCTTCTCCCTTACCTCTCCTTTC
-----+-----+-----+-----+-----+ 660
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[illegible]

[illegible]

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 1561 -----+-----+-----+-----+-----+-----+-----+ 1620
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 TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
 1621 -----+-----+-----+-----+-----+-----+-----+ 1680
 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGACG
 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGAA
 1681 -----+-----+-----+-----+-----+-----+-----+ 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAAGTTGATGTCGTCTT
 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC
 1741 -----+-----+-----+-----+-----+-----+-----+ 1800
 CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCC
 CACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCC
 1801 -----+-----+-----+-----+-----+-----+-----+ 1860
 GTGACGTCCTTGGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG
 TCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 1861 -----+-----+-----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCGTCCGGTTCAACGACTTAGTTACCTCG
 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCTTCCCATCCTCCTGACCACCGGGGC
 1921 -----+-----+-----+-----+-----+-----+-----+ 1980
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 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
 1981 -----+-----+-----+-----+-----+-----+-----+ 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA
 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG
 2041 -----+-----+-----+-----+-----+-----+-----+ 2100
 GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGAC
 GCACGGAACACACCTTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGC
 2101 -----+-----+-----+-----+-----+-----+-----+ 2160
 CGTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG
 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTA
 2161 -----+-----+-----+-----+-----+-----+-----+ 2220
 CCTGTACATGTCTCGAGCTCTTCATGATCACCGGTGCACCCGGCACGTGGAATTCGAAAT
 <---- 4.p53-BE
 (intron)
 GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCCTGGACAAGCCCTGAC
 2221 -----+-----+-----+-----+-----+-----+-----+ 2280
 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG
 ----->
 AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC
 2281 -----+-----+-----+-----+-----+-----+-----+ 2340
 TTCGGTTCGGTTTCCAGGCGAGGCCGCGCCCACTCACGCGCGGCGGGGCGCCCCCG
 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACG
 2341 -----+-----+-----+-----+-----+-----+-----+ 2400
 CCCCTCTCTCGGACGTCGGAAGTCTTGCTATAACGAGTAAAGACCGTCAAGAGTCTGC

10240-1024550
 10240-1024550

2401 TAGGAAATAAGTCAACCCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
-----+-----+-----+-----+-----+ 2460
ATCCTTTATTCAGTCGTGGCTTCGTCACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA

2461 TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
-----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

2521 TTTTATTGTCACACAGAAAAGGAAACTGCCTTGCTCTCCCTCCGGGAATTCTCTCTTTAA
-----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATT

2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGGTTTCTGCCCTTCTCTTTCT
-----+-----+-----+-----+-----+ 2640
CTGACATTCAGCGACGGACTCACCAAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

2641 TCTTTTGGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG
-----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCC

2701 TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
-----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT

2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
-----+-----+-----+-----+-----+ 2820
CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

2821 AGACGTG
----- 2827
TCTGCAC

T02410-1624E860

Fig. 10

<---- 1.p53-BE ---->
(promoter)

1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAATAACCTTTAGAGATGCCCCAACTGT 60
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 -->
 61 TTTCCCCAGAACACCAGCATTCAATAGGTGTTCAATAGATTCTTCAAAGGATTCCA 120
 AAAGGGGTCCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT
 121 AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCTTTGACATTAGCATAC 180
 TTCCGTTTCTTCAAACCCCTTGTCAATATATTAATGGGTGGGAACTGTAATCGTATG
 181 TAAGGGCCCTGAGAAGTTTGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT 240
 ATTCCCGGGACTCTTCAAACCTAATTCCTTTCAAAGTTTAATTTCAATTGGGTCTTAAA
 241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT 300
 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
 301 GAACCTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 360
 CTTGAACCTCTATTAATCTGCATGCACCCATCTCCCATCCCCTTCCCCCATACCGTATCT
 361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA 420
 TTCTCGTCCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->
(promoter)

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTTGTAAAG 480
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 481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCATAATTCATTCCTTCTAG
 541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT 600
 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
 601 CCTTTCCCTTTTTTCTCTCTTCCCTCCTTCCATTCTTCTTCCCTTACCTCTCCTTTC 660
 GGAAAGGGGAAAAAAGAGAGAGGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAAG
 661 CTTCCTCACACCCCTTTTCTTCTTCTTTTACATTTTTTTATTTAAATGAACCTTTTC 720
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAATGTAAAAAATAAATTTACTTGAAAAG
 721 ATTTTGAATAGTTTATAGGATTTCAAAAATTTGCAGAGATAATACAGAGAATGCCATA 780
 TAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

10240-162660

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841
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GGCTGGCACGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
841
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ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
901
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GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCCAACAGGCTCCAG
961
CACTACCTTTCCGGAGTCTCTCCATTGGATTGGATCTAACTCCCGGGTTGTCCGAGGTC
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1021
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1081
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CAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAAC
1141
GTCTCGAACCACCTGCTACGGTTTCTTATGACTTTGGAAATCACACAGGTCAGACCTTG
TGCATCCAAATTCAGGTTCACTAATGATGTCATTATCCAAACATACCTTCTGTAAATTC
1201
ACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAAG

----- 3.p53-BE -----
(promoter)
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1261
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CACCAGAGCACGAAAGAATTACAAGATTTTTTTTTTAAAGAAAATTGGCCAGGAAATAATG
1321
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AGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTGG
1381
TCATTGCTTCCTGTCTTCATTAACTTACAAATTATATCGACCCCGATACGCTAAACC
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1441
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AGAGCCTTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGAAACG
1501
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1561
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1621
GAAAGAGACTCACTGAGGTGCTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACGC
CTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCAGGTTGAAGTACAGCAGAAG
1681
GAGACTCGAGGTAAGAGGAAGTCTGGAGGGGTTGAAGGGTCCAAGTGTGCTCTTC

1741 CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCTCACCTGAAGTGAGCATGCCAGCC 1800
 -----+-----+-----+-----+-----+
 GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCGG
 1801 ACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCCT 1860
 -----+-----+-----+-----+-----+
 TGACGTCTTTCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA
 1861 CACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC 1920
 -----+-----+-----+-----+-----+
 GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGAGTTAGTTACCTCGG
 1921 CTCCCCAACC CGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCCTGACCACCGGGGCT 1980
 -----+-----+-----+-----+-----+
 GAGGGGTTGGGCCCCGAAGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA
 1981 TTTCTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC 2040
 -----+-----+-----+-----+-----+
 AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAAG
 2041 TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG 2100
 -----+-----+-----+-----+-----+
 ACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCCGTGACC
 2101 CACGGAACACACCCTGAGGCCAGCCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCG 2160
 -----+-----+-----+-----+-----+
 GTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCTCGACGGAGAAGAGGGCGC
 2161 GGTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTCACTTCGGAGGATTGCTCA 2220
 -----+-----+-----+-----+-----+
 CCAACCACCTGGGCGAGTCATGCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT
 2221 ACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG 2280
 -----+-----+-----+-----+-----+
 TGTGGTACGACCCGTAGACCTGGGAGGATGGAGACCCTAGGGAGAGGACGGGCCCCACC
 2281 AGGCTTACCCCGTCTTAGTCCCAGGGGATAGGCAAAGTGGGGCGGGCGCGGGACGCGTGCG 2340
 -----+-----+-----+-----+-----+
 TCCGAATGGGGCAGAATCAGGGCCCCCTATCCGTTTACCCCGCCCGCGCCCTGCGCACGC
 2341 GGATTGCGGCGGCAGCGGCGCACGCGGGCACCTGGGAGCGGGCGGGCTGCTGCGGGAGGCG 2400
 -----+-----+-----+-----+-----+
 CCTAACGCCCGCGTCGCCGCGTGCGCCCGTGGACCCTCGCCGCCCCGACGACGCCCTCCGC
 2401 TTGGAGACTGGCTCCCCGGGGCTGTTAGGACCTTCCTCAGGCCCGGGTGCTCAGAACGA 2460
 -----+-----+-----+-----+-----+
 AACCTCTGACCGAGGGCCCCCGACAATCCTGGAAGGGAGTCCGGGCCCCACGAGTCTTGCT
 2461 TGGAGGACTTGCTTTTCTTGGGCCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGG 2520
 -----+-----+-----+-----+-----+
 ACCTCCTGAACGAAAAGAACC CGGAACCTACGCTTCACGACTAGGGCGACCCGTCCGCCCC
 2521 CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA 2580
 -----+-----+-----+-----+-----+
 GTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAACTCCACCCGCACCCCCGCGCT
 2581 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGA 2640
 -----+-----+-----+-----+-----+
 GTCCTTAACCTTCGCCTTCAGACCCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT
 <----- 4.p53-BE ----->
 (intron)
 2641 GAGAGGAGCGGAACCTCCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC 2700
 -----+-----+-----+-----+-----+
 CTCTCCTCGCCTTGAGGACCTGTTCCGGACTGTTCCGGTTCGGTTTCCAGGCGAGGCCGCG

p53-4.1000000000000000

GGGTGGGTGAGTGC GCGCCGCCCCGCGGGGCGGGGAGAGAGCCTACAGCCTTCAGAACA 2701
-----+-----+-----+-----+-----+-----+ 2760
CCCCCCCACTCACGCGCGGGCGGGGCGCCCCGCCCCCTCTCTCGGATGTCGGAAGTCTTGT
CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG
2761 -----+-----+-----+-----+-----+ 2820
GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTCAC
GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTCTCGAAAAAGTTATATGGGGG
2821 -----+-----+-----+-----+-----+ 2880
CAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAGAAAGAGCTTTTTCAATATACCCCC
CTGAATGAGCTTCTGGAGGCTTGTATACCGTTTTTTATTGTCACACAGAAAAGGAACTG
2881 -----+-----+-----+-----+-----+ 2940
GACTTACTCGAAGACCTCCGAACAAATGGCAAAAAATAACAGTGTGTCTTTTCCTTTGAC
CCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC
2941 -----+-----+-----+-----+-----+ 3000
GGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACATTCAGCGACGGACTCACCAAAG
ATTTTGTTTTGTCTTCTGCCCCTTCTCTTTCTTTTCTTTTGGCCCTTTCTTAGCTTGCACTCC
3001 -----+-----+-----+-----+-----+ 3060
TAAACAAAACAAAAGACGGGAAGAGAAAGAAAGAAACGGGAAGAATCGAACGTGAGG
CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCACCGCACAGA
3061 -----+-----+-----+-----+-----+ 3120
GTACCACTAAAGACGAACCAGAGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT
ACCCGGCGCCTATTATTGGGCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC
3121 -----+-----+-----+-----+-----+ 3180
TGGGCGCGGATAATAACCGGTTCTTTGAACTCGTCGGACAAAACCTTTTCAGGGAGCGAG
AGAAATGCCAGCTTGCAGATGGCTAATCAAAG
3181 -----+-----+-----+-----+ 3212
TCTTTACGGTCGAACGTCTACCGATTAGTTTC

T02TH0" T02H0B00

Fig 11

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMI GG**AAA**AGCCCTGACAAGCCA

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2. p1140 IMII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMII GG**AAA**AGCCCTG**AAA**AGCCA

↑

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2280 (C→A)

3. p1140 IMIII

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIII GG**AAAT**CCCTG**AAAT**CCA

↑

↑

↑

↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2273 (G→T)

2280 (C→A)

2283 (G→T)

4. p1140 IMIV

p1140 GGACAAGCCCTGACAAGCCA

p1140 IMIV GCACAAGCCCT**C**ACAAGCCA

↑

↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

0934291 041201
T02T40 T62H860

Fig. 12

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG AAA ATCCCTG AAA ATCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2. p1141 1p53

p1141	AGAGATGCCCAAAGCTGTTTT
p1141 1p53	AGAGAT T CCCAA A ATGTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTTT
p1141 2p53	AATGTT T CTTAAG A TTTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

T00270 = T00270

p1141 AAACTACCTAAGAGCTATCT

p1141 3p53 ACAATACCTAAGAGCTATCT

 ↑ ↑

positions of the mutations (boldface and arrow): 1268 (A→C)
1270 (C→A)

5. p1141 Δ Bgl

<---- 1.p53-BE ---->
 p1141 AATAACCTTTAGAGATGCCCAAAC**TG**TTTTCCCCAGAACA
 p1141ΔBgl AATAACCTTTA-----GATCTCCCCAGAACA

6. p1141 ΔSpe

p1141 CATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTT
 p1141ΔBg1 CATCTTTGCCA-----CTAGTGGCTACATTT

7. p1141 Δ Mph

p1141 AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
p1141ΔBg1 AATTCATGCTATGCA-----TACCGTTCCAA

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
2228 (T→A)

2. p1142 IMIII

p1142 GGACAAGCCCTGACAAGCCA
p1142 IMIII GG**AA**ATCCCTGA**AA**ATCCA
 ↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)
2665 (G→T)
2672 (C→A)
2675 (G→T)

3. p1142 ΔBgl

<---- 1.p53-BE ---->
p1142 AATAACCTTTAGAGATGCCCCAACTGTTTTCCCCAGAACA
p1142ΔBgl AATAACCTTTA-----GATCTCCCCAGAACA

4. p1142 ΔSpe

<---- 2.p53-BE ---->
p1142 CATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTT
p1142ΔBgl CATCTTTGCCA-----CTAGTGGCTACATTT

5. p1142 ΔMph

<---- 3.p53-BE ---->

p1142

AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA

p1142ΔBg1

AATTCATGCTATGCA-----TACCGTTCCAA

09834291-041201

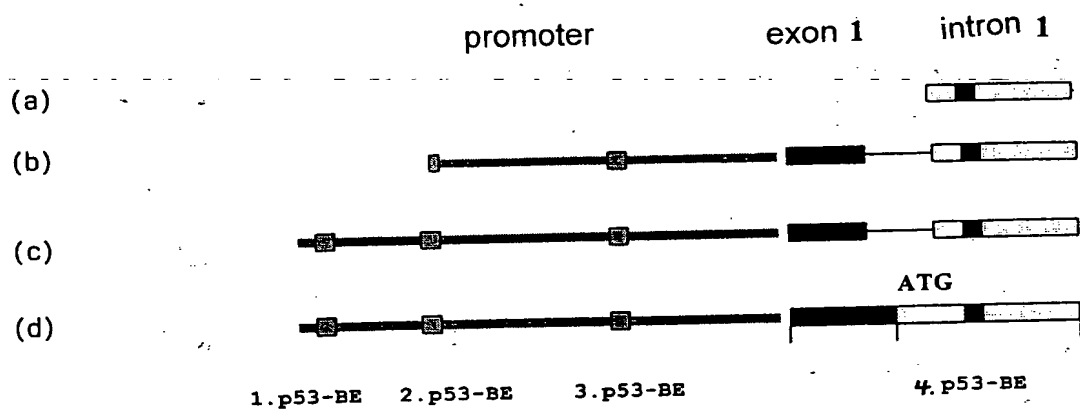


Fig. 14